

AMENDMENTS TO THE SPECIFICATION

Please amend the specification as specified below. No new matter has been added.

Page 9, second full paragraph:

The enzyme used in the process is preferably a mutant of P450_{cam} (such as mutant of the sequence shown in table 7; nucleic acid sequence is SEQ ID NO:1, amino acid sequence is SEQ ID NO:20) or a mutant of a naturally occurring homologue of P450_{cam}, typically of P450_{BM-3} from *Bacillus megaterium* (such as a mutant of the sequence shown in table 8; SEQ ID NO:2), P450_{terp} from *Pseudomonas sp*, and P450_{eryF} from *Saccharopolyspora erythraea*, and also P450 105 D1 (CYP105) from *Streptomyces griseus* strains. Note that the amino acid numbering shown in table 8 for P450_{BM-3} (SEQ ID NO:21) does not correspond to the numbering used in the description to denote mutations in this enzyme. The sequence shown in table 8 contains an additional amino acid at the N terminal. This is normally cleaved in vivo. Therefore each amino acid number shown in the table is always one more than the number used in the conventional numbering (as used in the description). The P450_{BM-3} sequence without the N-terminal methionine is SEQ ID NO:24.